

# SEQUENCE LISTING

SEQ ID NO: 1  
Sequence Length: 1013  
Sequence Type: Nucleic acid  
Stranded nos: Single  
Topology: Linear  
Molecular Type: cDNA

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GAATTCGGCA CGAGGGATCT GG ATG GCA TCT ACT TCG TAT GAC TAT TGC AGA 49
                        Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg
                        5 10
GTG CCC ATG GAA GAC GGG GAT AAG CGC TGT AAG CTT CTG CTG GGG ATA 97
Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile
                        15 20 25
GGA ATT CTG GTG CTC CTG ATC ATC GTG ATT CTG GGG GTG CCC TTG ATT 145
Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu Ile
                        30 35 40
ATC TTC ACC ATC AAG GCC AAC AGC GAG GCC TGC CGG GAC GGC CTT CGG 193
Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg
                        45 50 55
GCA GTG ATG GAG TGT CGC AAT GTG ACC CAT CTC CTG CAA CAA GAG CTG 241
Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu
                        60 65 70
ACC GAG GCC CAG AAG GGC TTT CAG GAT GTG GAG GCC CAG GCC GCC ACC 289
Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr
                        75 80 85 90
TGC AAC CAC ACT GTG ATG GCC CTA ATG GCT TCC CTG GAT GCA GAG AAG 337
Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys
                        95 100 105
GCC CAA GGA CAA AAG AAA GTG GAG GAG CTT GAG GGA GAG ATC ACT ACA 385
Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr
                        110 115 120
TTA AAC CAT AAG CTT CAG GAC GCG TCT GCA GAG GTG GAG CGA CTG AGA 433
Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg
                        125 130 135
AGA GAA AAC CAG GTC TTA AGC GTG AGA ATC GCG GAC AAG AAG TAC TAC 481
Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr
                        140 145 150
CCC AGC TCC CAG GAC TCC AGC TCC GCT GCG GCG CCC CAG CTG CTG ATT 529
Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Pro Gln Leu Leu Ile
                        155 160 165 170
GTG CTG CTG GGC CTC AGC GCT CTG CTG CAG TGA GATCCACGGA AGCTGGCACA 582
Val Leu Leu Gly Leu Ser Ala Leu Leu Gln ***
                        175 180 185
TCTTGAAGG TCCGTCCTGC TCGGCTTTTC GCTTGAACAT TCCCTTGATC TCATCAGTTC 642
TGAGCGGGTC ATGGGGCAAC ACGGTTAGCG GGGAGAGCAC GGGGTAGCCG GAGAAGGGCC 702
TCTGGAGCAG GTCTGGAGGG GCCATGGGGC AGTCCTGGGT TTGGGGACAC AGTCGGGTTG 762
ACCCAGGGCT GTCTCCCTCC AGAGCCTCCC TCCGACAAAT GAGTCCCCCC TCTTGTCTCC 822
CACCCGTAGA TTGGGCATGG GGTGCGGTGT GGGGGGCATG TGCTGCCTGT TGTTATGGGT 882
TTTTTTTGGC GGGGGGGTTG CTTTTTCTG GGGTCTTTGA GCTCCAAAAA AATAAACACT 942
TCCTTTGAGG GAGAGCACCA CACCTTAAAA AAAAAAAAAA AAAAAAAAAA AAAAAATTC 1002
GGGCGGCGCC C 1013

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SEQ ID NO: 2  
Sequence Length: 379  
Sequence Type: Nucleic acid  
Topology: Linear  
Molecular Type: cDNA  
Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCT AGT CAG GAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val	
15 20 25	
AAT ACT GCT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40 45	
CTG CTG ATC TAC TCG GCA TCC AAC CGG TAC ACT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg	
50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCT ACC TAC TAC TGC CAG CAA CAT TAT AGT	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser	
80 85 90	
ACT CCA TTC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 3  
Sequence Length: 418  
Sequence Type: Nucleic acid  
Topology: Linear  
Molecular Type: cDNA  
Sequence

ATG GAC TGG ACC TGG AGG GTC TTC TTG CTG GCT GTA GCT CCA GGT	48
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly	
-15 -10 -5	
GCT CAC TCC CAG GTG CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG	96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
-1 1 5 10	
CCT GGG GCC TCA GTG AAG GTT TCC TGC AAG GCA TCT GGA TAC ACC TTC	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	

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ACT CCC TAC TGG ATG CAG TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT      192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                               35                               40                               45
GAG TGG ATG GGA TCT ATT TTT CCT GGA GAT GGT GAT ACT AGG TAC AGT      240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
50                               55                               60
CAG AAG TTC AAG GGC AGA GTC ACC ATG ACC GCA AAG TCC ACG AGC      288
Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser
65                               70                               75
ACA GCC TAC ATG GAG CTG AGC AGC CTG AGA TCT GAG GAC ACG GCC GTG      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
80                               85                               90
TAT TAC TGT GCG AGA GGA TTA CGA CGA GGG GGG TAC TAC TTT GAC TAC      384
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
95                               100                               105
TGG GGG CAA GGG ACC ACG GTC ACC GTC TCC TCA G      418
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                               115                               120

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SEQ ID NO: 4

Sequence Length: 418

Sequence Type: Nucleic acid

Topology: Linear

Molecular Type: cDNA

Sequence

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ATG GAC TGG ACC TGG AGG GTC TTC TTC TTG CTG GCT GTA GCT CCA GGT      48
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
-15                               -10                               -5
GCT CAC TCC CAG GTG CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG      96
Ala His Ser Ser Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
-1 1                               5                               10
CCT GGG GCC TCA GTG AAG GTT TCC TGC AAG GCA TCT GGA TAC ACC TTC      144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15                               20                               25
ACT CCC TAC TGG ATG CAG TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT      192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                               35                               40                               45
GAG TGG ATG GGA TCT ATT TTT CCT GGA GAT GGT GAT ACT AGG TAC AGT      240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
50                               55                               60
CAG AAG TTC AAG GGC AGA GTC ACC ATC ACC GCA GAC AAG TCC ACG AGC      288
Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
65                               70                               75
ACA GCC TAC ATG GAG CTG AGC AGC CTG AGA TCT GAG GAC ACG GCC GTG      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
80                               85                               90
TAT TAC TGT GCG AGA GGA TTA CGA CGA GGG GGG TAC TAC TTT GAC TAC      384
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
95                               100                               105
TGG GGG CAA GGG ACC ACG GTC ACC GTC TCC TCA G      418
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                               115                               120

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